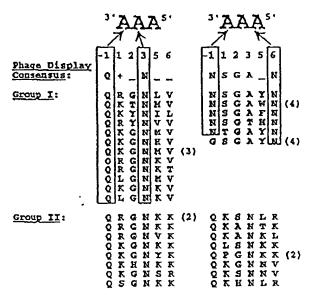
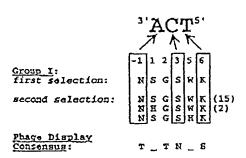


A. TATA Subsite Selection:



C. NRE Subsite Selection:



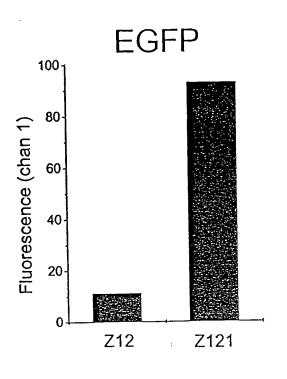
B. p53 Subsite Selection:

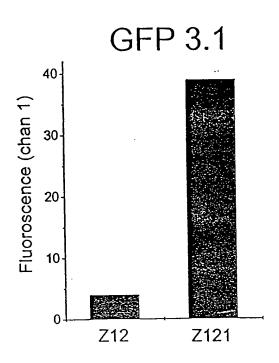
³'TGT⁵'				
Phage Display	-1 1 2 3 5 6 -1 1	2356		
Consensus:	H _ H H	. •		
Croup I:	HKHHKA (2) HLHHKA			
		R S S L V* Q S S K V*		
	QDNLKR WI	8 6 1 V* 9 8 8 R A*		
Group II:	ERWRNR EI	RWRNR (4) RWRNR RWRIR		
	ERWRRR EI	RWRSR		
	ERWRRR EI	RWRVR RWRVR		
		R W R V R R W R L R		
	EKWRRR (2) E1	KWRTR		
	ERWRKR (2) E	NWRKR Qwrkr Rwrmr		

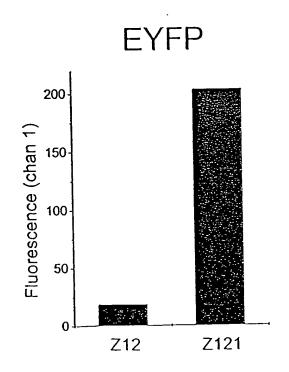
D. Group III Fingers:

	-1	1	2	3	5	6	-1	1	2	3	5	6	
From the													
TATA Solection:	R	R	W	L	x	L	R	ĸ	W	L	0	L	
	R	ĸ	H	L	ĸ	L							(2)
From the													
p53 Selection:	ĸ	ĸ	₩	L	R	L	R	x	W	L	М	L	
	ĸ	X	W	L	R	L	R	ĸ	W	Į	N	L	
	R	K	W	L	R	L	R	ĸ	W	Y	O	L	
	R	K	W	L	Ŕ	L					-		
From the													
NRE Selection:	ĸ	K	W	L	R	L	R	Α	W	·L	X	L	
	R	ĸ	W	L	K	L	K	K	W	Y	R	L	
	R	K	W	L	ĸ	L							

Behavior of different Fluorescent Proteins in the Bacterial Two-Hybrid System







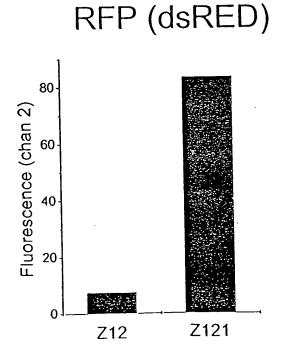
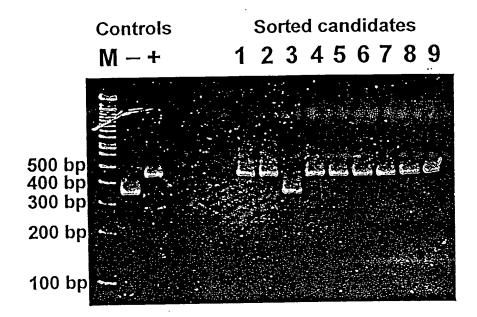


Figure 5.



(_)

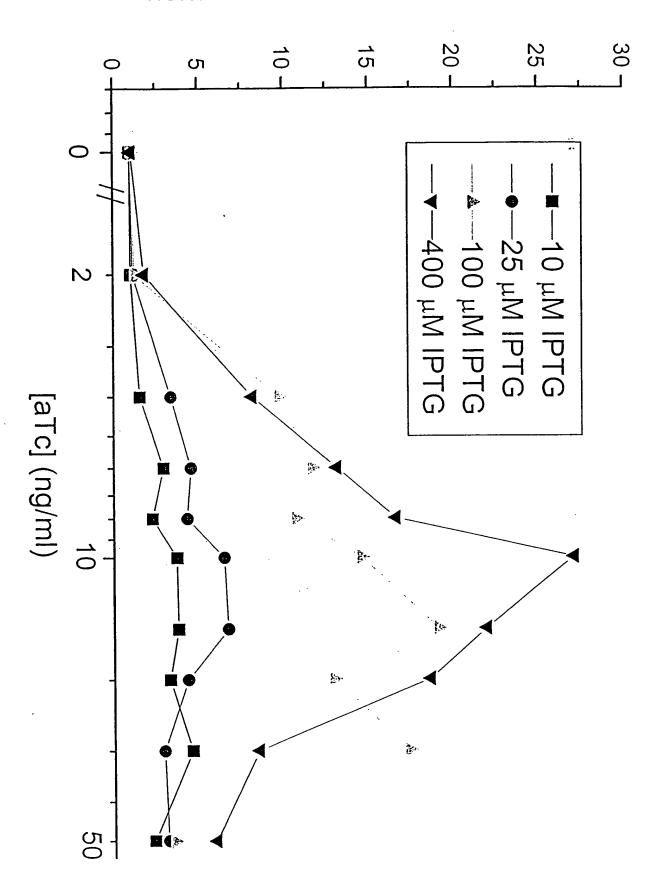
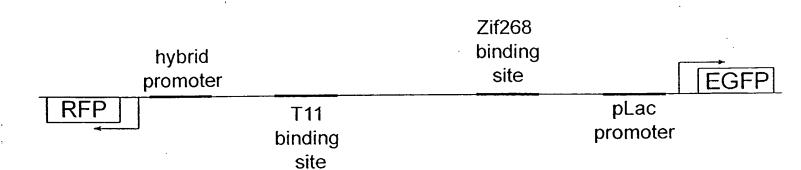
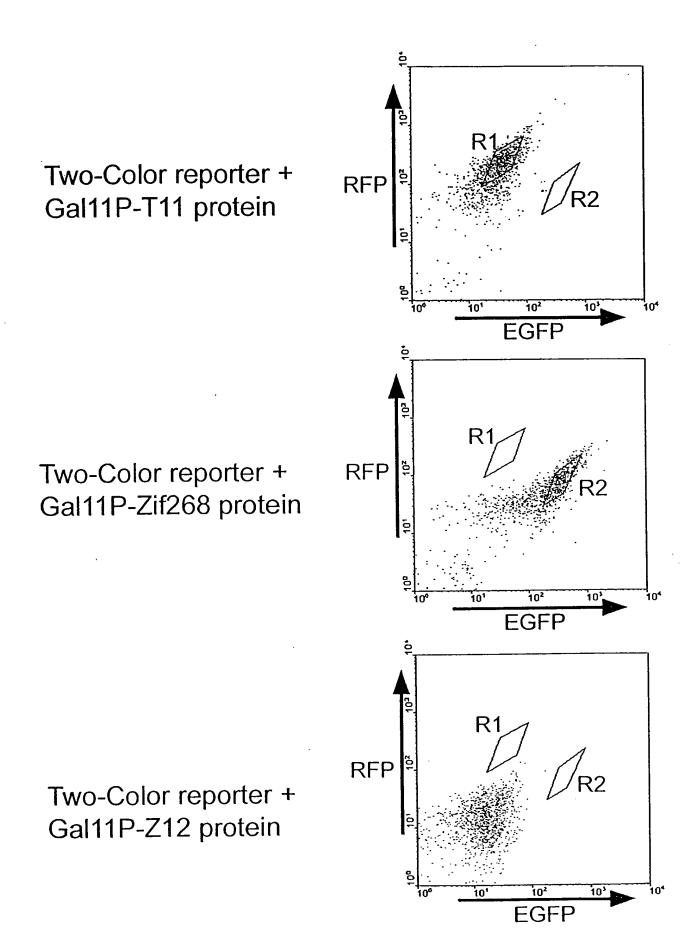


Figure 6

reporter construct #2

reporter construct #1





ì

Fig 9

P53^{ZF} in vitro site selection consensus sequence:

CXGGA<u>CACGT</u>X

(where X = no clear preference)

In vivo site selection library

CGGGA<u>NNNNN</u>G

(where N = a mixture of A, G, C, and T)

Selected Clones:

Sequence	# of clones
CGGGA <u>CACGT</u> G	9
CGGGA <u>CATGT</u> G	5
CGGGA <u>CACGG</u> G	2

Sequence	Fold Activation
CGGGA <u>CACGT</u> G	18.6±2.7
CGGGA <u>CATGT</u> G	12.0±0.5
CGGGACACGGG	12.6±1.9